

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 12:18:19 ; Search time 3320 Seconds
(without alignments)
2529.395 Million cell updates/sec

Title: US-09-765-034-2
Perfect score: 1747
Sequence: 1 MGIWAMNATCKNMLAEPN.....KSLTFSRWAEHLISFREK 334

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 segs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US0976503/rnat.05122002.132014.21397/app.query.fasta_1.519
-DB=Pending_Patents_NA.Main -QFMT=fastap -SUFFIX=p2n.rnrm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09765034.@cgn.1.1.1396.@rnat.05122002.132014.21397
-NCPU=6 -ICPU=3 -NO.XLPEXY -NO.MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA.Main:*
1: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*

29: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
84: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*
85: /cgn2_6/ptodata/1/pna/US0976503.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1747	100.0	1338	61	US-60-172-490-1	Sequence 1, Appl
2	1737	99.4	1005	18	US-09-416-760-37	Sequence 37, Appl
3	1737	99.4	1005	18	US-09-416-760A-37	Sequence 35, Appl
4	1737	99.4	1005	18	US-09-417-044-35	Sequence 35, Appl
5	1737	99.4	1005	33	US-09-875-076-35	Sequence 35, Appl
6	1737	99.4	1005	33	US-09-876-252-37	Sequence 37, Appl

```
8 1737 99.4 1436 1 PCT-US01-01316-36
9 1737 99.4 1436 1 PCT-US01-16450-1352
10 1737 99.4 1436 1 PCT-US01-16450A-1352
11 1737 99.4 1542 30 US-09-764-886-36
12 1737 99.4 1542 65 US-60-213-954-7
13 1737 99.4 1704 25 US-09-652-917-3485
14 1737 99.4 1704 29 US-09-726-175-3444
15 1737 99.4 4232 1 PCT-US01-01316-11
16 1737 99.4 4232 30 US-09-764-886-11
17 1725 98.7 1996 18 US-08-559-524-1
18 1725 98.7 1996 35 US-09-947-922-1
19 1720 98.5 1428 1 PCT-US96-00392A-1
20 1720 98.5 1428 11 US-08-781-456A-1
21 1720 98.5 1428 34 US-09-908-593-1
22 1713 98.1 4787 36 US-09-950-083-12061
23 1713 98.1 4787 40 US-10-105-299-14212
24 1713 98.1 197293 66 US-60-226-176-3
25 1713 98.1 197293 67 US-60-233-468-3
26 1713 98.1 197293 75 US-60-313-371-3
27 1709 97.8 1385 1 PCT-US00-09070-47
28 1709 97.8 1385 36 US-09-950-083-12257
29 1709 97.8 1385 40 US-10-105-299-2757
30 1708 97.8 4787 36 US-09-950-083-12062
31 1708 97.8 4787 40 US-10-105-299-14213
32 1700 97.3 4250 64 US-60-205-423-173
33 1700 97.3 4250 64 US-60-205-423-174
34 1700 97.3 4250 64 US-60-205-423-175
35 1700 97.3 4250 64 US-60-205-423-176
36 1689 96.7 1494 1 PCT-US01-08656-2075
37 1619 92.7 2518 66 US-60-229-515-1915
38 1571 89.9 1284 22 US-09-572-411-5769
39 1461 83.6 1137 17 US-09-347-127-72
40 1461 83.6 1137 34 US-09-905-059-72
41 1461 83.6 1138 18 US-09-471-275-5373
42 1461 83.6 1587 18 US-09-457-877-104
43 1461 83.6 1587 36 US-09-952-981-104
44 1231.5 70.5 1543 33 US-09-891-138A-1
45 1231.5 70.5 1564 80 US-60-360-207-14297
```

ALIGNMENTS

```
RESULT 1
US-60-172-490-1
; Sequence 1, Application US/60172490
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph
; APPLICANT: Lachowicz, Jean
; APPLICANT: Wang, Wei
; APPLICANT: Gustafson, Eric
; TITLE OF INVENTION: Adenosine Receptor
; FILE REFERENCE: CNO1084P
; CURRENT APPLICATION NUMBER: US/60/172,490
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1005)
US-60-172-490-1
```

Alignment Scores:

```
Pred. No.: 1,2e-151 Length: 1338
Score: 1747.00 Matches: 334
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 61 Gaps: 0
```

```
US-09-765-034-2 (1-334) x US-60-172-490-1 (1-1338)
1 MetLeuGIYIleMeTAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAla
1 ATGCGGGGAGTCATGCGATGGAATGCAATGCTCAAAAACCTGGCTGGCAGAGGCTGCC
21 LeuGIuLySTyTrpLeuSerIlePheTrpGlyIleGluPheValGlyValLeuGly
61 CCGGAAAGAGTACTACTTCCATTTTATATGAGATGAGATGCTGGTGGAGACTCTTGA
41 AsnTrpIleValValTyrGlyIlePheSerLeuLysAsnTrpAsnSerSerIle
121 AATACCATGTGTGTACGGCTACATCTTCTCTGAAAGAACTGGAAACAGCATATAT
61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle
181 TATCTCTTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr
241 AGGAGTTATGCGCAATGGAAGTATATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTG
101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg
301 GTGCTTCATGCGCAACCTCTATACAGCATCTCTTCTGCTGCTGCTGCTGCTGCTGCTG
121 TyrLeuIleIleLeuTyrProPheArgGluHisLeuGlnLysGluPheAlaIle
361 TACTGTAAATTAATTAATACCTCTTCGAGAGACCTTCGCAAAAAGAGTTCTATT
141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu
421 TTAATCTCTGCGCATTTGGCTTTTATGACTTAAGAGTTACTACCATCTTCCCTT
161 IleAsnProValIleThrAspAsnGlyThrPheCysAsnAspPheAlaSerSerLysp
461 ATAATCTCTGTTATACGATGACATGCAACCTTAATGATTGTCGAAGTTCTGGAAC
181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu
541 CCCACATCAACCTCATTTAGAGCATGTGTCATACAGCTGGGTTCTTATTCCTCTT
201 PheValMetCysPhePheTyrTrpLysIleAlaLeuPheLeuLysGlnArgAsnArgGln
601 TTTGTGATGTGTTCTTTATATACAGATGCTCTCTCTTAAGCAGAGATAGCAG
221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValAlaIle
661 GTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu
721 TTCCTGTGCGCTTTAGACCCATCATGCGGATGAGAGATGAGATGCTTACGCGCTG
261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr
781 GGGAGTTGGAAGCATATACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA
840 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyasp
861 CCGGCTTTGGCTTTCTGTAACAGTGTCAACACCTGCTCTCTATTTCTTTGGAGAT
901 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe
961 CACTTCAGAGCATGCTGATGATCAACTGAGACACAACTCAATCCCTTACATCCTTT
321 SerArgTrpAlaHisGluLeuLeuSerPheArgGluLys 334
961 AGCAGATGGGCTCATGAACTCTACTTTCATTCACAGAGAAAG 1002
```

RESULT 2

US-09-416-760-37

```
Sequence 37, Application US/09416760
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Brulisma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huang T.
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Re
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/416,760
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/152,524
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/151,114
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/108,029
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
```

```
SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-416-760-37

Alignment Scores:
Pred. No.: 7,05e-151 Length: 1005
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x US-09-416-760-37 (1-1005)

QY 1 MetLeuGlyTlIeMeKAlaTrpAsnAlaTrpCysLysAsnTrpLeuAlaIaGluAlaIa 20
DB 1 ATGCTGGGATCATGCGATGGAATGCACACTTGCACAAAGCTGCGACAGAGCGTCC 60
QY 21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValAlaGlyValLeuGly 40
DB 61 CTGGAAAAGTACTACTCTTCCATTCTTTATGGATTTGAATTGCTTGGAGTCTTGGAA 120
QY 41 AsnThrIleValAlaTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
DB 121 AATACCATTTGTTTATGCGTACATCTTCTCTGACAAAGCTGGAACAGCATATATT 180
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 181 TATCTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
DB 241 AGGAGTTATGCCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 300
QY 101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 301 GTGCTTCATGCAACCTCATACACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 121 TyrLeuIleIleLysTyrTrpPheArgGluHisLeuLeuGlnLysGluPheAlaIle 140
DB 361 TACTTGATATTAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGlnLeuProIleLeuProLeu 160
DB 421 TTAATCTCTTGGCCATTGGGTTTATGTAACCTTAGATTACTACCACTTCTCTCT 480
QY 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
DB 481 ATAAATCGTGTATATACATGACATGACACACTGTAATGATTTTGCAGTTCTGAGAC 540
QY 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
DB 541 CCCAACTACACCTCATTTACAGCATGTCTTAACACTCTTGGGCTTCTTATTCCTCT 600
QY 201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysIleArgAsnArgGln 220
DB 601 TTGTGATGTGTTCTTTATTAACAAGATTGCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValAlaIle 240
DB 661 GTTGCTACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
DB 721 TTCTCTGTGCTTTTACACCTATCAGCTCATGCGGAATGAGGATCCCTTACCCCTG 780
QY 261 GlySerTrpLysGluTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
DB 781 GGGAGTTGAGACGATATGACGTGACCTGAGTGCTGATCATCACTCTTATCATGTGACA 840
```

```
Oy 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuGlyAsp 300
      |||||
Db 841 CGGCTTTGGCTTTCTTGACAGTGTCAACACCTGCTTTATTTCTTTGGAGAT 900
Oy 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPhelySerLeuThrSerPhe 320
      |||||
Db 901 CACTTCAGAGGACATGCTGTATGAATCACTGACAGACAACTCAATTCCTTACATCCTTT 960
Oy 321 SerArgTTPAlaHisGlnLeuLeuLeuSerPheArgGlyLys 334
      |||||
Db 961 AGCAGATGGGCTCATGAACCTCTACTTTCATTCAGAGAAAG 1002

RESULT 3
US-09-416-760A-37
; Sequence 37, Application US/09416760A
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Brünsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Re
; FILE REFERENCE: ARPN-0054
; CURRENT APPLICATION NUMBER: US/09/416, 760A
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
```

```
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-416-760A-37

Alignment Scores:
Pred. No.: 7,05e-151 Length: 1005
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
Gaps: 0

US-09-765-034-2 (1-334) x US-09-416-760A-37 (1-1005)
Oy 1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaGlnAla 20
      |||||
Db 1 ATGCTGGGGATCATGGCATGGAATCACTTGCAAAAACCTGGCTGACAGAGCTGCC 60
Oy 21 LeuGluLysTyrTrpLeuSerIlePheTyrGlyIleGluPheValGlyValLeuGly 40
      |||||
Db 61 CTGCAAAAGTACTACCTTCCATTTTATGAGATGAGTGGCTGGTGGATCCTTGGA 120
Oy 41 AsnThrIleValIleValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerAsnIle 60
      |||||
Db 121 AATACCATGTTGTTAGGCTACATCTTCTCTGAGAAAGTGAAGACAGATATATT 180
Oy 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPrometLeuIle 80
      |||||
Db 181 TATCTCTTAACCTCTCTGCTGACTTACCTTTCTGTGCACCTCCCATGCTGATA 240
Oy 81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
      |||||
Db 241 AGGAGTTATGCCAATGGAACTGGATATATGAGACGTGCTGCATATAGCAACCGATAT 300
Oy 101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
      |||||
Db 301 GTGCTCATGCAACCTCTATACCAAGCATTTCTTTTCACATTTTATACGATATGCA 360
Oy 121 TyrLeuIleIleLysTyrTrpPheArgGlnHisLeuLeuGlnLysGluPheAlaIle 140
      |||||
Db 361 TACTTGATTAATTAAGTATCCCTTCCGAGAACACCTTTCGAAAAGAAAGATTGCTATT 420
Oy 141 LeuIleSerLeuAlaIleTrpValLeuValIleThrLeuGluLeuLeuProIleLeuProLeu 160
      |||||
Db 421 TTAATCTCTGGCCATTGGGTTTATGTAACCTTAGAGTTACATACCATATCTTCCCTT 480
Oy 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
      |||||
Db 481 ATTAATCTCTTATATACGACAAATGGCCACCTGTAATGATTTTTCGAAGTTCTGGAGAC 540
Oy 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
      |||||
Db 541 CCCAACTCAACCTCATTTACGACATGTGTACACACTGTGGGGTCTTATATCTCTT 600
Oy 201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
      |||||
```

Db	601	TTTGAGAGCTGTTCTTTATTAACAAGATTGCTCTCTCTTAAGCAGGAGAAATAGGCAC	660
Qy	221	ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValIle	240
Db	661	GTTCGTACTGCTCGCCCTTGAAACCCCTCCAACTTGCTCATCATGGCAGGTAAATC	720
Qy	241	PheserValProPheThrProTyrHisValMetArgAsnValArgIleAsSerArgLeu	260
Db	721	TTTCCTGTGCTTTTAAACCTTAACCATGCGATGGGAATGTAGGAATGCGTTACGCGT	780
Qy	261	GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr	280
Db	781	GGGAGTTGGAAAGCAGTATCAGTGCAGCTCAGGCTGCTCATCACTCCTTTTACATTGTGACA	840
Qy	281	ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp	300
Db	841	CGGCGTTTGGCCTTTCGTAACAGTGCATCAACCCCTGCTCATATTTCTTTGGGAGAT	900
Qy	301	HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe	320
Db	901	CACCTCAGGGAGCAGTCGATGTAACAACCTGAGACCAACTTCAAAATCCCTTACATCCTTT	960
Qy	321	SerArgTrpAlaHisGluLeuLeuLeuSerPheArgLysLys	334
Db	961	AGCGATATGGCTCATGAACCTCTCACTTTCATCATGGAATAAAG	1002

US-09-417-044-35
; Sequence 35, Application US/09417044

```

: GENERAL INFORMATION:
: APPLICANT: Chen, Ruoping
: APPLICANT: Dang, Huang T.
: APPLICANT: Liaw, Chen W.
: APPLICANT: Lin, T-Lin
: TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
: FILE REFERENCE: AREN0050
: CURRENT APPLICATION NUMBER: US/09/417,044
: CURRENT FILING DATE: 1999-10-12
: Prior application data removed - consult PALM or file wrapped
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 35
: LENGTH: 1005
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-417-044-35

```

Alignment Scores:	
Pred. No.:	7,056-151
Score:	1737.00
Percent Similarity:	99.708
Best Local Similarity:	99.708
Query Match:	99.438
DB:	18
Length:	1005
Matches:	333
Conservative:	0
Mismatch:	1
Indels:	0
Gaps:	0

US-09-765-034-2 (1-334) x US-09-417-044-35 (1-1005)

Qy	1	MelleuGgylIleMeIaIatrpShaIaIathCysIySaSntrPleuAaIaIaIuIaIa	20
	11		
	21		
	31		
	41		
	51		
	61		
	71		
	81		
	91		
	101		
	111		
	121		
	131		
	141		
	151		
	161		
	171		
	181		
	191		
	201		
	211		
	221		
	231		
	241		
	251		
	261		
	271		
	281		
	291		
	301		
	311		
	321		
	331		
	341		
	351		
	361		
	371		
	381		
	391		
	401		
	411		
	421		
	431		
	441		
	451		
	461		
	471		
	481		
	491		
	501		
	511		
	521		
	531		
	541		
	551		
	561		
	571		
	581		
	591		
	601		
	611		
	621		
	631		
	641		
	651		
	661		
	671		
	681		
	691		
	701		
	711		
	721		
	731		
	741		
	751		
	761		
	771		
	781		
	791		
	801		
	811		
	821		
	831		
	841		
	851		
	861		
	871		
	881		
	891		
	901		
	911		
	921		
	931		
	941		
	951		
	961		
	971		
	981		
	991		
	1001		
	1011		
	1021		
	1031		
	1041		
	1051		
	1061		
	1071		
	1081		
	1091		
	1101		
	1111		
	1121		
	1131		
	1141		
	1151		
	1161		
	1171		
	1181		
	1191		
	1201		
	1211		
	1221		
	1231		
	1241		
	1251		
	1261		
	1271		
	1281		
	1291		
	1301		
	1311		
	1321		
	1331		
	1341		
	1351		
	1361		
	1371		
	1381</		

QY	81	ArgerterYrAlaasnGlysantrPlietGlyGlyspAlleuGysliIseeranAgtYr	100
QY	241	AGGAGTATGGCAATGGAAACTGGATATATGGAAACCTGCTCGCATATACCAACCGATAT	300
QY	101	ValleuHsAlaasnLeuYrThSerlleuPheLeuThrPheIleSerlleAsParg	120
Db	301	GTCGTCATGGCAACCTCTATACAGCATTCCTCTTCTCACTTTTATACAGATATGATCGA	360
QY	121	TyrLeuIlelleuYsTYrTYrProPheargGlnHsleuLeuGlnYsLysgluPheAlaIle	140
Db	361	TACTGTATTAATTAAGTATACCTTTCGAGAAACACCTCTCGCAAAAAGAAAGATTGTATT	420
QY	141	LeuIleSerleuAlaIleTrpValleuValThreuGluLeuLeuProIleuProleu	160
Db	421	TTAATCCCTGGCCATTGGGTTTGTATACCTTAAGATTACTACCACTATCCCTT	480
QY	161	IleasnProValIleThrAspAsnGlyThrThrcysAsnAspPheAlaSerSerGlyAsp	180
Db	481	ATTAATCCTGTTATTAAGTACGACAAATGGCAACCACTGTATGATGTTTTGCCAAGTTCTGGAGAC	540
QY	181	ProasnTYrAsnLeuIleTYrSerMetCysLeuThrLeuLeuGlyPheleuIleProleu	200
Db	541	CCCAATACAAACCTCATTTACAGCATGTGTCATACACTGTGGGGTTCCTATTCTCTT	600
QY	201	PheValMetCysPhePheTYrTYrLysIleAlaLeuPheLeuYsGlnArgAsnArgGln	220
Db	601	TTTGTGATGTGTTCTTTATTATACAAATATGCTCTCTCCATAAAGCAGAGAAATAGGCAG	660
QY	221	ValIaThrAlaLeuProleuGlnLysProleuAsnleuValIleMetAlaValIle	240
Db	661	GTTCATACGTGTCGCCCTTGAAACCCCTCAACTGGTCATCATAGGAGTGTATATC	720
QY	241	PheSerValProPheThrProTYrHisValMetArgAsnValArgIleAlaSerArgLeu	260
Db	721	TTTCCTGCGTTTTTACACCCTATACAGTATGGGGAATGTAGAGATCGGTTACGCGTCG	780
QY	261	GlySerTrpLysGlnTYrGlnCysThrGlnValIleAsnSerPheTYrIleValThr	280
Db	781	GGGAGTTGGAAAGCATATACGTACGACATCAGGTCTCATCAACTCTTTACATGTGTACA	840
QY	281	ArgProleuAlaPheLeuAsnSerValIleAsnProValPheTYrPheLeuLeuGlyAsp	300
Db	841	CGGCGCTTGGCTTTCGAAACAGTGTATCAACCTCTCTCTATATTTCTTTGGGGAGAT	900
QY	301	HisPheArgAspMetIleMetAsnGlnLeuArgHisAsnPheYsSerLeuThrSerPhe	320
Db	901	CACATTCAGGAGCATGCTGATATATCAACACTGAGACACAACTTCAAAATCCCTTACATCCTTT	960
QY	321	SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGlnLys	334
Db	961	AGCAGATGGCGTCATGAAGCTCTCTTCTTCAATCGAGAAAG	1002

RESULT 5
HE-09-875-076-35

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/136,436
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/136,437
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/136,439
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/136,567
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/137,127
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/137,131
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/141,448
: PRIOR FILING DATE: 1999-06-29
: PRIOR APPLICATION NUMBER: 60/156,653
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/156,633
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/156,555
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/156,634
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/157,280
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,294
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,281
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,293
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,282
: PRIOR FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 35
: LENGTH: 1005
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-765-076-35

Alignment Scores:
Pred. No.: 7,05e-151 Length: 1005
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
Gaps: 0
DB: 33

US-09-765-034-2 (1-334) x US-09-875-076-35 (1-1005)

QY 1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAla 20
DB 1 ATGCTGGGAGCATGCGATGCAATGCACTTGCAGAAACCTGCTGCGACGAGCTGCC 60
QY 21 LeuGluLysTyrTyrLeuSerIlePheSerLeuLysAsnTrpAsnTrpLeuAla 40
DB 61 CTGGAAAGAGTACTACCTTCCATTTTATGAGATGAGTGGTGGAGTCCCTTGA 120
QY 41 AsnThrIleValIleTyrGlyTyrIlePheSerLeuLysAsnTrpAsnTrpLeuAla 60
DB 121 AATACCATTTGTTTACGGCTACATCTTCTCTGGAAGAACTGGAACAGATATATT 180
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysTrpIleuPrometLeu 80
DB 181 TATCTCTTAACCTCTGCTGCTGACTTACCTTTCTGTGACACCCCTCCATGCTGATA 240
QY 81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
DB 241 AGGAGTATATGCAATGGAATGATATATGAGACGCTCTGATTAAGCAACGATAT 300
QY 101 ValLeuHisAlaAsnLeuTyrThrSerIleuPheLeuThrPheIleSerIleAspArg 120
```

```

DB 301 GTGCTTATGCCAACCTCTAATACGACATCTCTTTCACCTTTATGACATGATCGA 360
QY 121 TyrLeuIleIleLysTyrProPheArgLysIleLeuGlnLysGluPheAlaIle 140
DB 361 TACTGATATATTAATATACCTTTCGAGACACCTTTCGAAAAAAGAGTTCTATT 420
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuProIleLeuProLeu 160
DB 421 TTAATCTCTTGGCCATTTGGGTTTAACTTAACCTTAAGATTAACCATCTCCCTT 480
QY 161 IleAsnProValIleThrAspAsnGlyThrPheCysAsnAspPheAlaSerSerLysp 180
DB 481 ATAATTCCTGTTATACGACATGACACCTTAATGATTTTGCAGATTCGGAAC 540
QY 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuGlyPheLeuIleProLeu 200
DB 541 CCCACATCAACCTCATTTACAGCATGATGTCATCAACATGTTGGGTTCTTATCTCTT 600
QY 201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgLys 220
DB 601 TTGTGATGTGTTCTTTATTAACAAAGATGCTCTCTTCAACAGAGAAATAGCGAG 660
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValIle 240
DB 661 GTTGCTTACTGCTCTGCCCCCTGAAAGCCCTCAACCTTGTCATCATGCGATGTAATC 720
QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
DB 721 TTCTGTGCTTTTACACCCATATCAGTCATGCGGAATGAGAGATGCTTACAGCGCTG 780
QY 261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
DB 781 GGGAGTGGAAAGCAGTACAGTACAGCTCAGGCGTCAACCACTCTTTTACATGTGTGACA 840
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLysp 300
DB 841 CGGCTTTGGCTTCTCTAACAAGTCTCATCAACCTGCTCTTCTTATTTCTTTGGAGAT 900
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
DB 901 CACTTCAGGAGCATGCTGATGATCACTGAGACACCACTCAATTCCTTACATCCTTT 960
QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgLysp 334
DB 961 AGCAGATGGGCTCATGAACTCTTACTTTCATTCAGAGAAAG 1002

RESULT 6
US-09-876-252-37
: Sequence 37, Application US/09876252
: GENERAL INFORMATION:
: APPLICANT: Behan, Dominic P.
: APPLICANT: Lehmann-Brulsma, Karin
: APPLICANT: Chalmers, Derek T.
: APPLICANT: Lowitz, Kevin P.
: APPLICANT: Lin, I-Lin
: APPLICANT: Dang, Huang T.
: APPLICANT: Chen, Ruoping
: APPLICANT: Liaw, Chen W.
: TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled
: FILE REFERENCE: AREN-0054
: CURRENT APPLICATION NUMBER: US/09/876,252
: PRIOR FILING DATE: 2001-06-07
: PRIOR APPLICATION NUMBER: 09/416,760
: PRIOR FILING DATE: 1999-10-12
: PRIOR APPLICATION NUMBER: 09/170,496
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: 60/110,060
: PRIOR FILING DATE: 1998-11-27
: PRIOR APPLICATION NUMBER: 60/120,416
: PRIOR FILING DATE: 1999-02-16
: PRIOR APPLICATION NUMBER: 60/121,852
: PRIOR FILING DATE: 1999-02-26
: PRIOR APPLICATION NUMBER: 60/109,213
```

```

: PRIOR FILING DATE: 1998-11-20
: PRIOR APPLICATION NUMBER: 60/123,944
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,945
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,948
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,951
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,946
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/123,949
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/152,524
: PRIOR FILING DATE: 1999-09-03
: PRIOR APPLICATION NUMBER: 60/151,114
: PRIOR FILING DATE: 1999-08-27
: PRIOR APPLICATION NUMBER: 60/108,029
: PRIOR FILING DATE: 1998-11-12
: PRIOR APPLICATION NUMBER: 60/136,436
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/136,439
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/136,567
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/137,127
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/137,131
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/141,448
: PRIOR FILING DATE: 1999-06-29
: PRIOR APPLICATION NUMBER: 60/136,437
: PRIOR FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/156,555
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/156,634
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/156,653
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: 60/157,280
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,294
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,281
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/157,282
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/156,633
: PRIOR FILING DATE: 1999-09-29
: NUMBER OF SEQ ID NOS: 146
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 37
: LENGTH: 1005
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-876-252-37

Alignment Scores:
Pred. No.: 7.05e-151 Length: 1005
Score: 1737.00 Matches: 333
Percent Similarity: 99.708 Conservative: 0
Best Local Similarity: 99.708 Mismatches: 1
Query Match: 99.43% Indels: 0
DB: 33 Gaps: 0

US-09-765-034-2 (1-334) x US-09-876-252-37 (1-1005)
QY 1 MetLeuGlyIleKetalaTrpAnaIaThrCysLysAsnTrpLeuAlaIaIaIaIa 20
DB 1 ARGCTGGGATCATGCGATGAGATGCAACTGCGAGCGAGCGAGCGAGCGAGCG 60
QY 21 LeuGluLysTyrTrpLeuSerIlePheTyrGlyIleGluPheValAlaGlyValLeuGly 40

```

```

DB 61 CTGGAAAGTACTACCTTCATTTTATGGAGTTGAGTCTGTGGAGCTTGCA 120
QY 41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSera 60
DB 121 AATACCATTTGTTGTACGGCTACATCTTCTCTGAAGACGAGCAACAGCATTA 180
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPromLeu 80
DB 181 TATCTCTTAACCTCTGCTGCTGACTAGCTTTCTTGCGACCTCCCAAGCTGATA 240
QY 81 ArgSerTyrAlaAsnLysAsnTrpIleTyrGlyAspValLeuLysIleSerAsn 100
DB 241 AGGAGTTATGCGCAATGAACTGGATATATGAGAGCTGCTGCATTAACCAACG 300
QY 101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle 120
DB 301 GTGCTTCATGCCAAGCTGATACAGCATTTCTTCTCTTATTCACAGATAGATCG 360
QY 121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysGluPheAla 140
DB 361 TACTGTATATTAAGTATCTTCCGAGAACACCTTCTGCAAAAGAGATTGCTATT 420
QY 141 LeuIleSerLeuAlaIleTyrPheValLeuValThrLeuGluLeuLeuProIle 160
DB 421 TTAATCTCTTGGCATTTGGGTTTATGTAACCTTAGAGTACTACCAATCTCCCT 480
QY 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheIleSerSeri 180
DB 481 ATTAATCCCTGTATTAATGAGCATGACACACCTGTAATGATTTTGCAGTTCTG 540
QY 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIle 200
DB 541 CCCAAGTACAACTCATTTTACAGCATGTGCTTAACCTGTGGGTTCTTATTCCT 600
QY 201 PheValMetCysPhePheTyrTyrIleAlaLeuPheLeuLysGlnAsnArg 220
DB 601 TTTGTATGTGTTCTTTATTAACAAGATTGCTCTCTCTTAAGAGAGAAATAG 660
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaVal 240
DB 661 GTTGCTACTGCTGTGCGCCCTGTAAGCCCTGCACTGCTCATGCGAGTGAAT 720
QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSer 260
DB 721 TTTCTGTGCTTTTACACCCATGACGATCGGAATGTGAGATTCGCTTACCC 780
QY 261 GlySerTrpLysGlnIleGlnCysThrGlnValIleAsnSerPheTyrIleVal 280
DB 781 GGGAGTTGGAAGCATATCATGCTCACTGAGTGTATCAATCTTTTACATTGTG 840
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuGly 300
DB 841 CGGCTTTGGCTTTCTGGAACATGTCATCAACCCGTCTTATTTCTTTGGGAG 900
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuTr 320
DB 901 CACTTCAGGAGCATGCTGATGATCAACAGAGACACAACTCAATCCCTTATC 960
QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
DB 961 AGCAGATGGGCTCATGAATCTTACTTTCATTCAGAGAAAG 1002

RESULT 7
PCT-US01-01316-36
: Sequence 36, Application PCT/US0101316
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc., et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PTO202PCT
: CURRENT APPLICATION NUMBER: PCT/US01/01316
: PRIOR FILING DATE: 2001-01-14
: PRIOR application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 88

```

```

; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-01316-36

Alignment Scores:
Pred. No.: 1,11e-150 Length: 1436
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x PCT-US01-01316-36 (1-1436)

QY 1 MetLeuGlyIleMeTAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
DB 93 ATGCTGGGAGATCATGGCATGGAATGCAACTTGCAGAAAGCTGGCGACAGAGGCTGCC 152
QY 21 LeuGluLysTrpTrpLeuSerIlePheTrpGlyIleGluPheValValGlyValLeuGly 40
DB 153 CTGGAAGAAGTACTACCTTTCCATTTTATGGAGATTGAGTTGCTTGAGGAGCTCTTGA 212
QY 41 AsnThrIleValValTrpGlyTrpIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
DB 213 AATACCATTTGTTTGTAGCGGTACATCTTCTCTGAAAGAACTGGAGACAGCATATATT 272
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 273 TATCTCTTTAACCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATA 332
QY 81 ArgSerTrpAlaAsnGlyAsnTrpIleTrpGlyAspValLeuCysIleSerAsnArgTyr 100
DB 333 AGGAGTTATGCGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 392
QY 101 ValLeuHisAlaAsnLeuTrpThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 393 GTCCTTCATGCGCAACCTCTATACAGCATCTTCTCTGAAAGAACTGGAGACAGCATATATT 452
QY 121 TyrLeuIleIleLysTrpProPheArgGluHisLeuLeuGlnLysLeuGluPheAlaIle 140
DB 453 TACTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 512
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
DB 513 TTAATCTCTGCGCATTTGGGTTTATGAACTTACAGAGTTACCATTTCTCCCTT 572
QY 161 IleAsnProValIleThrAspAsnGlyThrTrpCysAsnAspPheAlaSerSerGlyAsp 180
DB 573 ATAAATCTCTGTTATTAATGACATGACATGACATGACATGACATGACATGACATGACATGAC 632
QY 181 ProAsnTrpAsnLeuIleTrpSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
DB 633 CCCACATCAACACCTATTTACAGCATGCTCTCAACACCTGTTGGGTTCTTCTCTCTT 692
QY 201 PheValMetCysPhePheTrpTrpLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
DB 693 TTTTGAGATGTTCTTTTATTAACAAGATGCTCTTCTTCAACAGAGAGATGAGGAG 752
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
DB 753 GTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
QY 241 PheSerValIleProPheThrProTrpHisValMetArgAsnValArgIleAlaSerArgLeu 260
DB 813 TTCTCTGCTGCTTTTACACCTCATATCATATGCGGAATGAGAGATGCTTTCAGGCTG 872
QY 261 GlySerTrpLysGlnTrpGlnCysThrGlnValValIleAsnSerPheTrpIleValThr 280
DB 873 GGAAGTTGGAAGAGATATCAGTGCACAGTGCATCACTCTTTTACATTTGTGACA 932
```

```

QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTrpPheLeuLeuGlyAsp 300
DB 933 CGGCTTTGGCTTTCTGTGAACAGTGTATCAACACCTGCTCTTCTTATTTCTTTGGAGAT 992
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
DB 993 CACTTCAGGACATGCTGTGTGAATCAACTGACACACAACTTCAAAATCCCTTATCATCTTT 1052
QY 321 SerArgTrpAlaHisGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 334
DB 1053 AGCAGATGGGCTCATGACACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1094

RESULT 8
PCT-US01-16450-1352
; Sequence 1352, Application PC/TUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1352
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-16450-1352

Alignment Scores:
Pred. No.: 1,11e-150 Length: 1436
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: Gaps: 0

US-09-765-034-2 (1-334) x PCT-US01-16450-1352 (1-1436)

QY 1 MetLeuGlyIleMeTAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
DB 93 ATGCTGGGAGATCATGGCATGGAATGCAACTTGCAGAAAGCTGGCGACAGAGGCTGCC 152
QY 21 LeuGluLysTrpTrpLeuSerIlePheTrpGlyIleGluPheValValGlyValLeuGly 40
DB 153 CTGGAAGAAGTACTACCTTTCCATTTTATGGAGATTGAGTTGCTTGAGGAGCTCTTGA 212
QY 41 AsnThrIleValValTrpGlyTrpIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
DB 213 AATACCATTTGTTTGTAGCGGTACATCTTCTCTGAAAGAACTGGAGACAGCATATATT 272
QY 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 273 TATCTCTTTAACCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATA 332
QY 81 ArgSerTrpAlaAsnGlyAsnTrpIleTrpGlyAspValLeuCysIleSerAsnArgTyr 100
DB 333 AGGAGTTATGCGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 392
QY 101 ValLeuHisAlaAsnLeuTrpThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 393 GTCCTTCATGCGCAACCTCTATACAGCATCTTCTCTGAAAGAACTGGAGACAGCATATATT 452
QY 121 TyrLeuIleIleLysTrpProPheArgGluHisLeuLeuGlnLysLeuGluPheAlaIle 140
DB 453 TACTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 512
QY 141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
DB 513 TTAATCTCTGCGCATTTGGGTTTATGAACTTACAGAGTTACCATTTCTCCCTT 572
```



```
QY 161 ILeasnProvalIlethraspasnglyThrThrcysasnasphealaserSerglyasp 180
Db 573 ATAAATCCCTTTATTAATGACAAATGGACACACCTGTATATATTTGGAAAGTTGGAGAC 632
QY 181 ProasnTyranleuiletyrSerMetCysLeuThreuleuglyPheleuileProleu 200
Db 633 CCCAACTACACCTCATTTACAGCATGTCTTAACACTGTGGGGTCTTATTCCTCTT 692
QY 201 PheValMetCysPhepheytyrTylysIleAlaLeuPheleuysglnArasArargln 220
Db 693 TTGTGTATGTTCTTTATTTACAAAGATGTCTCTCTCTTAAGAGAGAAATAGGCAG 752
QY 221 ValAlaThrAlaLeuProleuglyLysProleuAsnLeuValIleMetAlaValAlaIle 240
Db 753 GTTGCTACATGCTGTGCCCTTGAAAGCCCTCAACTGTGTATCAATGAGGAGGTATATC 812
QY 241 PheSerValPropherhrProtyrHisValMetArgasnaValArgIleAlaserArgleu 260
Db 813 TTCTCTGTGCTTTTACACCTTATCACGTATGCGGATGTGAGATCGCTTACGCGCTG 872
QY 261 GlySerTrpLysGlnTyrgIncystrGlnValAlaIleAsnSerPheTyrlleValThr 280
Db 873 GGGAGTTGGAAGACATATGATGACACTGACGTGTATCAACTCTTTTACATTGTGACA 932
QY 281 ArgProleuAlaPheleuAsnSerValIleAsnProValPheTyrrPheleuLeuglyasp 300
Db 933 CGGCCCTTGGCCTTTCTGAAACAGTGCATCAACCCGTCTTCTATTTCTTTTGGGAGAT 992
QY 301 HisPheArgspMetleuMetlaSnglnLeuArgHisasnPhelysserleuThrSerPhe 320
Db 993 CACTTCAGGACATGCTGATGAATCAACTGACACACACTTCACATTCCTTACATCCTTT 1052
QY 321 SerArgTrpAlaHisglnLeuLeuLeuSerPheArgglnLys 334
Db 1053 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAG 1094

RESULT 9
PCT-US01-16450A-1352
; Sequence 1352, Application PC/TUS0116450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL31PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1352
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-16450A-1352

Alignment Scores:
Pred. No.: 1,11e-150 Length: 1436
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: 1 Gaps: 0

US-09-765-034-2 (1-334) x PCT-US01-16450A-1352 (1-1436)
QY 1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpPheAlaIleAlaAla 20
Db 93 ATGCTGGGATCATGCGATGGAATGCAAACTGCAAAACCTGGGACAGAGAGCTGCC 152
QY 21 LeuGlnLysTyrrTyrrLeuSerIlePheTyrglyIleGlnPheValAlaIleValLeuGly 40
Db 153 CTGGAAGAAAGTACCTTTTTCATTTTATGCGATTGAGTTCGTTGCGGAGTCTTGGA 212
```

```
QY 41 AsnThrIleValValTyrglyTyrrIlePheSerleuLysAsnTrpAsnSerSerglyasp 60
Db 213 AATACCATTTGTTTATGAGGCTCATCTTCTCTGTGAAGAACAGAACACATATAT 272
QY 61 TyrLeuPheAsnLeuSerValIleSerAspLeuAlaPheleuysThrleuPrometleuIle 80
Db 273 TATCTCTTAACTCTCTGTCTGTACTTACTTCTTCTGTGACCCCTCCCAATGCTGATA 332
QY 81 ArgSerTyrrAlaAsnGlyAsnTrpIleTyrglyAspValLeuGlyIleSerAsnArgTyrr 100
Db 333 AGGAGTATGCAATGGAATGGAATGATATGAGAGCTGTCTGCAATACCAACCATAT 392
QY 101 ValLeuHisAlaAsnLeuTyrrThrSerIleleuPheleuThrPheIleSerrIleAspArg 120
Db 393 GTGCTTATGCAACCTCTTATACAGCATCTCTTCTCTCACTTTTATCACATAGATGGA 452
QY 121 TyrleuIleleuTyrrPropherArgGlnHisleuLeuGlnLysglnPheAlaIle 140
Db 453 TACTGTAAATTAAGATTCCTTCCGAAACCCCTTGTGCAAAAGAAAGATTGCTATT 512
QY 141 LeuIleSerleuAlaIleTrpValleuValThrleuGlnleuLeuProIleleuProleu 160
Db 513 TTATATCCTTGGGCATTTGGGTTTATAGTAACTTATAGTTACTACCATCTCCCTT 572
QY 161 ILeasnProvalIlethraspasnglyThrThrcysasnasphealaserSerglyasp 180
Db 573 ATAAATCCCTTTATTAATGACAAATGGACACACCTGTATATATTTGGAAAGTTGGAGAC 632
QY 181 ProasnTyranleuiletyrSerMetCysLeuThreuleuglyPheleuileProleu 200
Db 633 CCCAACTACACCTCATTTACAGCATGTCTTAAACACTGTGGGGTCTTATTCCTCTT 692
QY 201 PheValMetCysPhepheytyrTylysIleAlaLeuPheleuysglnArasArargln 220
Db 693 TTGTGTATGTTCTTTATTTACAAAGATGTCTCTCTCTTAAGAGAGAAATAGGCAG 752
QY 221 ValAlaThrAlaLeuProleuglyLysProleuAsnLeuValIleMetAlaValAlaIle 240
Db 753 GTTGCTACATGCTGTGCCCTTGAAAGCCCTCAACTGTGTATCAATGAGGAGGTATATC 812
QY 241 PheSerValPropherhrProtyrHisValMetArgasnaValArgIleAlaserArgleu 260
Db 813 TTCTCTGTGCTTTTACACCTTATCACGTATGCGGATGTGAGATCGCTTACGCGCTG 872
QY 261 GlySerTrpLysGlnTyrgIncystrGlnValAlaIleAsnSerPheTyrlleValThr 280
Db 873 GGGAGTTGGAAGACATATGATGACACTGACGTGTATCAACTCTTTTACATTGTGACA 932
QY 281 ArgProleuAlaPheleuAsnSerValIleAsnProValPheTyrrPheleuLeuglyasp 300
Db 933 CGGCCCTTGGCCTTTCTGAAACAGTGCATCAACCCGTCTTCTATTTCTTTTGGGAGAT 992
QY 301 HisPheArgspMetleuMetlaSnglnLeuArgHisasnPhelysserleuThrSerPhe 320
Db 993 CACTTCAGGACATGCTGATGAATCAACTGACACACACTTCACATTCCTTACATCCTTT 1052
QY 321 SerArgTrpAlaHisglnLeuLeuLeuSerPheArgglnLys 334
Db 1053 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAG 1094

RESULT 10
US-09-764-886-36
; Sequence 36, Application US/09764886
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
```

```
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-886-36

Alignment Scores:
Pred. No.: 1,11e-150 Length: 1436
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: 30 Gaps: 0

US-09-765-034-2 (1-334) x US-09-764-886-36 (1-1436)

QY 1 MetLeuGlyIleMeLaLaTRpAsnaLaThrCysLysAsnTRpLeuAlaIaIaIa 20
DB 93 ATGCTGGGATCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 152
QY 21 LeuGluLysTYrTYrLeuSerIlePheTYrGlyIleGluPheValIaGlyValLeuGly 40
DB 153 CTGGAAGAAGTACTACTCTTCCATTTTATGGGATGAGTTCGTTGGGAGTCTTGA 212
QY 41 AsnThrIleValIaTYrGlyTYrIlePheSerLeuLysAsnTRpAsnSerSerSnIle 60
DB 213 AATACCAATGTTGTTTACGGCTACATCTTCTCTGGAAGAACCTGGAACGAGTAATAT 272
QY 61 TYrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 273 TATCTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 332
QY 81 ArgSerTYrAlaAsnGlyAsnTRpIleTYrGlyAspValLeuCysIleSerAsnArgTYr 100
DB 333 AGGAGTTATGCCAAAGAAAGCAATGATATGAGACGTCCTCGATAGCAACCGATAT 392
QY 101 ValIleuHsAlaAsnLeuTYrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
DB 393 GTGCTTCAATGCCAACCTCTATACAGCATTTCTTCTCTCTCTCTCTCTCTCTCTCT 452
QY 121 TYrLeuIleIleLysTYrProPheArgLysIleLeuGlnLysIleLysGluPheAlaIle 140
DB 453 TACTTGATTAATTAAGTACCTCTTCCGAGAACCTCTGCAAAAGAAAGAGTTCTGCTANT 512
QY 141 LeuIleSerLeuAlaIleTYrValLeuValIleThrLeuGluLeuLeuProIleLeuProLeu 160
DB 513 TTAATCTCTCTGGCCATTTGGGTTTGTAGTAACCTTAGAGTTCTACCACTTCTCCCTT 572
QY 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
DB 573 ATTAATCTCTGTTATATGACATGACATGACACCTCTGTAATGATTGGCAAGTTCTGGAGAC 632
QY 181 ProAsnTYrAsnLeuIleTYrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
DB 633 CCCAACCTAACCTCATTTAGACATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 692
QY 201 PheValMetCysPhePheTYrTYrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
DB 693 TTTGGAGATGTTTCTTTATATGCAAGATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 752
QY 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMeLaIaValIaIle 240
DB 753 GTTGGTACTGCTCTGCCCCCTGGAAGCCCTCAACTGTTGTCATATGAGCAGTGAATATC 812
QY 241 PheSerValProPheThrProTYrHisValMeLaArgAsnValArgIleAlaSerArgLeu 260
DB 813 TTTCTCTGCTGTTTATACACCCATACAGCTCATGCGGAATGTAGAGATGCTTCAAGCCTG 872
QY 261 GlySerTrpLysGlnTYrGlnCysThrGlnValValIleAsnSerPheTYrIleValThr 280
DB 873 GGGAGTTGGAAGAGATACAGTACGACCTAGGCTGATCACTCTTTACATTTGTGACA 932
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTYrPheLeuLeuGlyAsp 300
DB 932 ATGCTGTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 332
```

```
DB 933 CGGCTTTGGCCCTTCTGACAGTGTATCAACCTGCTCTCTATTTCTTTGGAGAT 992
QY 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
DB 993 CACTTCAGGAGCATGCTGATGATGATCACTGACAGACACCACTTCAATTCCTTACATCTTT 1052
QY 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
DB 1053 ACCAGATGGGCTCATGCACTCTACTTTCATTCAGAGAAAG 1094

RESULT 11
US-60-213-954-7
; Sequence 7, Application US/60213954
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April
; APPLICANT: Nguyen, Dannel B.
; APPLICANT: Gandhi, Ameena R.
; APPLICANT: Kallick, Deborah A.
; APPLICANT: Griffin, Jennifer A.
; APPLICANT: Yue, Henry
; APPLICANT: Khan, Farrah A.
; APPLICANT: Patterson, Chandra
; APPLICANT: Lu, Dyung Alma M.
; APPLICANT: Tribouley, Catherine M.
; APPLICANT: Lu, Yan
; APPLICANT: Walla, Narinder K.
; APPLICANT: Graul, Richard
; APPLICANT: Yao, Monique G.
; APPLICANT: Yang, Junning
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0131 P
; CURRENT APPLICATION NUMBER: US/60/213,954
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO: 3485895CB1
US-60-213-954-7

Alignment Scores:
Pred. No.: 1,21e-150 Length: 1542
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: 65 Gaps: 0

US-09-765-034-2 (1-334) x US-60-213-954-7 (1-1542)

QY 1 MetLeuGlyIleMeLaLaTRpAsnaLaThrCysLysAsnTRpLeuAlaIaIaIa 20
DB 198 ATGCTGGGATCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 257
QY 21 LeuGluLysTYrTYrLeuSerIlePheTYrGlyIleGluPheValIaGlyValLeuGly 40
DB 258 CTGGAAGAAGTACTACTCTTCCATTTTATGGGATGAGTTCGTTGGGAGTCTTGA 317
QY 41 AsnThrIleValIaTYrGlyTYrIlePheSerLeuLysAsnTRpAsnSerSerSnIle 60
DB 318 AATACCAATGTTGTTTACGGCTACATCTTCTCTGGAAGAACCTGGAACGAGTAATAT 377
QY 61 TYrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
DB 378 TATCTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
QY 81 ArgSerTYrAlaAsnGlyAsnTRpIleTYrGlyAspValLeuCysIleSerAsnArgTYr 100
DB 437 ATGCTGTTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 332
```

```
|||||
Db 438 AGGAGTTATGCCATGAACTGGATATATGAGACGTGCTGCATACCAACCGATAT 437
Qy 101 ValLeuHISAlaAsnLeuYrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
Db 498 GTGCTTCATGCCCACTCTATACAGCATCTCTTCTCTCATCTTTATACATAGATCGA 557
Qy 121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
Db 558 TACTGTATATTAAGTATCTCTTCCGGAACACCTTCTGCAAAAGAAAGAGTTGCTAT 617
Qy 141 LeuIleSerLeuAlaIleTrrPValLeuValThrLeuGlnLeuLeuProIleLeuProLeu 160
Db 618 TTATCTCTCTGGCCATGGGTTTATAGTACCTTAGAGTTACTACCCATACCTCCCTT 677
Qy 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
Db 678 ATAAATCCTGTATTAAGTATGACATGGACACCACTGTATATGATTTTGCAGATCTCGAGAC 737
Qy 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
Db 738 CCCAATACCACTCATTTACACATGTGTAAACACTGTGGGGTCTTATTCCTCTT 797
Qy 201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
Db 798 TTTCGTATGTCTTTTATTTATTAAGATTTGCTCTCTCTTAAGCAGAGAAATAGGCAG 857
Qy 221 ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValAlaIle 240
Db 858 GTTGCTACGCTGCTGCCCTTGAAGCCCTCCTCACTGGTCAATGAGAGTGTATATC 917
Qy 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
Db 918 TTCTGTGTGTTTATACCCCTATACGTCATCGCATCGGATGTGAGATCGCTTACCGCTG 977
Qy 261 GlySerTrrPlySglnTyrGlnCysThrGlnValIleAsnSerPheTyrIleValThr 280
Db 978 GGGAGTTGGAGAGATATGCTGACCTCAGGTGCTCATCACTTATCATTTATGATGACA 1037
Qy 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
Db 1038 CGGCTTTGGCTTTCGAAACAGTGCATCAACCCGTCTTCTATTTCTTTGGGAGAT 1097
Qy 301 HisPheArgAspMetLeuMetAsnGlnLeuValArgHisAsnPheLysSerLeuThrSerPhe 320
Db 1098 CACTGTAGGAGCATGCTGATGAATCAACTGAGACACACAATCAAACTTACATCCTTT 1157
Qy 321 SerArgTrrAlaHisGlnLeuLeuLeuSerPheArgGlnLys 334
Db 1158 AGCAGATGGGCTCATGAACTCTACTTTCATTCAGAGAAAG 1199

RESULT 12
US-09-652-917-3485
; Sequence 3485, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holsteman, Douglas A.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600,1170-001
; CURRENT APPLICATION NUMBER: US/09/652,917
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3485
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(1704)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-917-3485

Alignment Scores:
pred. No.: 1,38e-150 length: 1704
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
DB: 25 Gaps: 0

US-09-765-034-2 (1-334) x US-09-652-917-3485 (1-1704)
Qy 1 MetLeuGlyIleMetAlaTrrPAsnAlaThrCysLysAsnTrrPLeuAlaIleGluAlaIle 20
Db 138 ATGCTGGGAGTATGATGGATGAAATGCAACTGCAAAATCGGTGGAGAGAGGCTGCC 197
Qy 21 LeuGlnLysTyrTrrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
Db 198 CTGGAAGAGTACTACCTTTCATTTTATGGATTTGAGTTCGTGGGAGTCTTGGA 257
Qy 41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrrPAsnSerSerAsnIle 60
Db 258 AATACCATTTGTTTATAGGCTACATCTCTCTGCAAGAACTGGAACACAGTATATT 317
Qy 61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
Db 318 TATCTCTTAACTCTCTGCTGCTGACTTAGCTTTTCTGCAACCCCTCCCATGGGATA 377
Qy 81 ArgSerTrrAlaAsnGlnAsnTrrPleTyrGlyAspValLeuLysIleSerAsnArgTyr 100
Db 378 AGGAGTTATGCCAATGGAATGATATATGAGACCTGCTGCAATACCAACCGATAT 437
Qy 101 ValLeuHISAlaAsnLeuYrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
Db 438 GTGCTTCATCCCACTCTTATACAGCATCTCTTCTCATCTTTATACATAGATCGA 497
Qy 121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
Db 498 TACTGTATATTAAGTATCTCTTCCGGAACACCTTCTGCAAAAGAAAGATTGCTAT 557
Qy 141 LeuIleSerLeuAlaIleTrrPValLeuValThrLeuGlnLeuLeuProIleLeuProLeu 160
Db 558 TTATCTCTCTGGCCATTTGGGTTTATGTAACCTTAAGTACTACCAATACCTCCCTT 617
Qy 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
Db 618 ATAAATCCTGTATTAAGTATGACATGGACACCACTGTATATGATTTTGCAGATCTGGAGAC 677
Qy 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
Db 678 CCCAATACCACTCATTTATACAGATGTGTCTAACAATGTGGGTTCTTATTCCTCTT 737
Qy 201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
Db 738 TTTCGTATGTCTTTTATTTATCAAGATGCTCTCTCTTAAGCAGAGAAATAGGCAG 797
Qy 221 ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValAlaIle 240
Db 798 GTTGCTACGCTCTGCCCTTGAAGCCCTCCTCACTGGTGCATCAAGAGTGTATATC 857
Qy 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
Db 858 TTCTGTGTGTTTATACCCCTATACAGTATGAGATGTGAGATCGTTACGCGCTG 917
Qy 261 GlySerTrrPlySglnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
Db 918 GGGAGTTGGAGAGATATGCTGACCTCAGGTGCTCATCACTCTTATCATTTGATGACA 977
Qy 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
Db 978 CGGCTTTGGCTTTCGAAACAGTGTATCAACCTGTCTTCTATTTCTTTGGGAGAT 1037
```

QY 301 HispHeaGASPmetLeuMetasnglnLeuAArgHIsasnPhelySerLeuTherSerPhe 320
| | | | |
Db 1038 CACTTCAGGAGCATGCTGATGATCAACAGACACCAACTCAATCCCTTATCCCTT 1097
QY 321 SerArgTPAlaHisGlnLeuLeuSerPheArgGlnLys 334
| | | | |
Db 1098 AGCAGATGGGCTCATGATGACTCTTCTTCTTCTGAGAGAAAG 1139
RESULT 13
US-09-726-175-3444
; Sequence 3444, Application US/09726175
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Donovan, Michael J.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600,2054-001
; CURRENT APPLICATION NUMBER: US/09/726,175
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/167,859
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 3770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3444
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1704)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-175-3444
Alignment Scores:
Pred. No.: 1,38e-150 Length: 1704
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
Gaps: 0
DB: 29
US-09-765-034-2 (1-334) x US-09-726-175-3444 (1-1704)
QY 1 MetLeuGlyIleMetAlaTPRpsnAlaThrCysLysAsnTPRLeuAlaAlaGlnAlaAla 20
| | | | |
Db 138 ATGCTGGGAGCATGCGATGAGATGCAACTTGCAAAACTGGCTGGCAGACAGGCTGCC 197
QY 21 LeuGlnLysTPRTPRLeuSerIlePheThyGlyIleGlnPheValAlaGlyValLeuGly 40
| | | | |
Db 198 CTGGAAGAGTACCTTCCATTTTATGAGATGAGTTCGTTGCTGGAGTCTCTTGA 257
QY 41 AsnThrIleValIleValTPRTPRLeuSerIlePheSerLeuLysAsnTPRpsnSerSerIle 60
| | | | |
Db 258 AATACCATGTTGTTTACGCGCTACATCTTCTCTGAGAGAACTGAGACAGCAGTAATAT 317
QY 61 TyrLeuPheAsnLeuSerValSerIlePheLeuAlaPheLeuCysThrLeuProMetLeuIle 80
| | | | |
Db 318 TATCTCTTAACCTCTGCTGCTCAGCTTAGCTTTCTGTGACCCCTCCCATGCTGATA 377
QY 81 ArgSerTPRAlaAsnGlyAsnTPRTPRLeuThyGlyAspValLeuCysIleSerAsnArgTyr 100
| | | | |
Db 378 AGGAGTATGCTCAATGCAATGAGATGATATGAGACGCTCTCTGATTAAGCAACCGATAT 437
QY 101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
| | | | |
Db 438 GTGCTTCATGGCAACCTTATACAGCAGCAATCTCTTCTCATTATAGCATTAAGCATGCA 497
QY 121 TyrLeuIleIleLysTyrPhePheArgGlnHisLeuLeuGlnLysGlnPheAlaIle 140
| | | | |
Db 498 TACTTGATTAATTAAGTATCTTTCGAGACACCTTTCGCAAAAGAAAGAGTTCTCTATT 557

QY 141 IleuIleSerLeuAlaIleTPRValLeuValThrLeuGlnLeuProIleLeuProLeu 160
| | | | |
Db 558 TTAATCTCTGTCGCACTTTGGCTTTAGTAACCTTAGAGTTAGACTACCACTTCCCTT 617
QY 161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
| | | | |
Db 618 ATTAATCCCTGTTATTAACCTACAAATGGACACCCTGTAATGAATTTTGCAGAGTTCTGGAGAC 677
QY 181 ProAsnTPRAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
| | | | |
Db 678 CCCAATCAACCTCATTTTACAGCATGTCTTACACCTTTGGGGTCTTCTTCTCTT 737
QY 201 PheValMetCysPhePheThyTyrIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
| | | | |
Db 738 TTTGTGATGCTGTTCTTTTATTAACAAGATTGCTCTCTTCTTAAACAGAGAAATGAGCAG 797
QY 221 ValAlaIleThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValAlaIle 240
| | | | |
Db 798 GTTGCTACTGCTGCTGCCCTTGAAGAGCTCTCAACTTGGTATGATGGAGTGGTAATC 857
QY 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
| | | | |
Db 858 TTCTCTGCTCTTTTACACCTTATCAGCATGCGGAATGTAGATGCTTACAGCCTG 917
QY 261 GlySerTPRPLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
| | | | |
Db 918 GCGAGTTGGAACAGATACATGACAGTCACTGAGTGCATCACTCTTTTACATTTGAGACA 977
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
| | | | |
Db 978 CGGCTTTGGCTCTTCTGAAAGTGTCAACCAACCTGCTCTTATTTCTTTTGGAGAT 1037
QY 301 HisPheArgASPmetLeuMetasnglnLeuAArgHIsasnPhelySerLeuTherSerPhe 320
| | | | |
Db 1038 CACTTCAGGAGCATGCTGATGATCAACAGACACCAACTCAATCCCTTATCCCTT 1097
QY 321 SerArgTPRAlaHisGlnLeuLeuSerPheArgGlnLys 334
| | | | |
Db 1098 AGCAGATGGGCTCATGATGACTCTTCTTCTTCTGAGAGAAAG 1139
RESULT 14
PCT-US01-01316-11
; Sequence 11, Application PC/TUS0101316
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT202PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01316
; CURRENT FILING DATE: 2001-01-14
; Prior application data removed - refer to PALM or file wrapper
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4232
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US01-01316-11
Alignment Scores:
Pred. No.: 4,36e-150 Length: 4232
Score: 1737.00 Matches: 333
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.43% Indels: 0
Gaps: 0
DB: 1
US-09-765-034-2 (1-334) x PCT-US01-01316-11 (1-4232)
QY 1 MetLeuGlyIleMetAlaTPRpsnAlaThrCysLysAsnTPRLeuAlaAlaGlnAlaAla 20
| | | | |
Db 103 ATGCTGGGAGCATGCGATGAGATGCAACTTGCAAAACTGGCTGGCAGACAGGCTGCC 162


```

Db 883 GGGAGTTGGAGCAGTATCATGCACGTCGTCATCACTCCTTTACATTGTGACA 942
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyasp 300
    |||||||
Db 943 CGGCTTTGGCCTTTCTGAAACAGTGTCAATCAACCCGTCTTCTATTTCTTTGGGAGAT 1002
QY 301 HisPheArgAspMetLeuMetLeuAsnGlnLeuArgHisAsnPhelySerLeuThrSerPhe 320
    |||||||
Db 1003 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACCTCAAAATCCCTTACATCCTTT 1062
QY 321 SerArgTrrPAlaHisGlnLeuLeuSerPheArgGluLys 334
    |||||||
Db 1063 AGCAGATGGGCTCATGAACCTCTACTTTCATTCAAGAGAAAAG 1104

```

Search completed: December 9, 2002, 13:22:55
 Job time : 3346 secs